

SEQUENCE LISTING

<110> Hauer, Bernhard
 Schmid, Rolf D.
 Schwaneberg, Ulrich

<120> Electron donor system for enzymes and its use in the biochemical
 conversion of substrates

<130> M/40076

<140> US 10/031,241

<150> PCT/EP00/07251
 <151> 2000-07-27

<160> 35

<170> PatentIn Ver. 2.1

<210> 1
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 <212> DNA
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<220>
 <223> Description of the artificial sequence:
 Oligonucleotide for genomic Bacillus
 megaterium DNA

<400> 1
 gtgaaagagg gatcccatga caattaaaga aatgcc 36

<210> 2
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 Oligonucleotide for genomic Bacillus
 megaterium DNA

<400> 2
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<210> 3
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<220>
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<400> 3
 gtacgtgatt ttgcaggag

<210> 4
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sequencing

<400> 4
ggctatcatg cgatgatggt 20

<210> 5
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<223> Description of the artificial sequence: Primer for
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cccagcttat gatgaaaac 19

<210> 6
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<210> 8
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<210> 24

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<211> 36
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 Oligonucleotide for tag at C terminus

<400> 24
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 Oligonucleotide for tag at C terminus

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<400> 28
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<400> 29
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<400> 31
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<223> Description of the artificial sequence: Primer for
 P450 BM-3 point mutant F87A

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<210> 33
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 <212> DNA
 <213> Artificial sequence

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 1 5 10 15
 aat tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa 96
 Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
 20 25 30
 att gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt 144
 Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
 35 40 45
 gta acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat 192
 Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
 50 55 60
 gaa tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt 240
 Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg

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65	70	75	
gat ttt gca gga gac ggg tta ttt aca agc tgg acg cat gaa aaa aat			288
Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn			
80	85	90	95
tgg aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca			336
Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala			
	100	105	110
atg aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt			384
Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val			
	115	120	125
caa aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa			432
Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu			
	130	135	140
gac atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac			480
Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn			
	145	150	155
tat cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca			528
Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr			
	160	165	170
agt atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca			576
Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala			
	180	185	190
aat cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa			624
Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu			
	195	200	205
gat atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc			672
Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg			
	210	215	220
aaa gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac			720
Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn			
	225	230	235
gga aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc			768
Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg			
	240	245	250
tat caa att att aca ttc tta att gcg gga cac gaa aca aca agt ggt			816
Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly			
	260	265	270
ctt tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta			864
Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu			

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275	280	285	
caa aaa gca gca gaa gaa gca gca cga gtt cta gta gat cct gtt cca			912
Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro			
290	295	300	
agc tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac			960
Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn			
305	310	315	
gaa gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca			1008
Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala			
320	325	330	335
aaa gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac			1056
Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp			
340	345	350	
gaa cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg			1104
Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp			
355	360	365	
gga gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt			1152
Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser			
370	375	380	
gcg att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg			1200
Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala			
385	390	395	
tgt atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt			1248
Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly			
400	405	410	415
atg atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg			1296
Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu			
420	425	430	
gat att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa			1344
Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys			
435	440	445	
gca aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act			1392
Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr			
450	455	460	
gaa cag tct gct aaa aaa gta cgc aaa aag gca gaa aac gct cat aat			1440
Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn			
465	470	475	
acg ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga			1488
Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly			

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480	485	490	495	
acg gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg	1536			
Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro				
500	505	510		
cag gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga	1584			
Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly				
515	520	525		
gct gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac	1632			
Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn				
530	535	540		
gca aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta	1680			
Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val				
545	550	555		
aaa ggc gtt cgc tac tcc gta ttt gga tgc ggc gat aaa aac tgg gct	1728			
Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala				
560	565	570	575	
act acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct	1776			
Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala				
580	585	590		
aaa ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac	1824			
Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp				
595	600	605		
gac ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac	1872			
Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp				
610	615	620		
gta gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa	1920			
Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys				
625	630	635		
tct act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt	1968			
Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu				
640	645	650	655	
gcg aaa atg cac ggt gcg ttt tca acg aac gtc gta gca agc aaa gaa	2016			
Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu				
660	665	670		
ctt caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa	2064			
Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu				
675	680	685		
ctt cca aaa gaa gct tct tat caa gaa gga gat cat tta ggt gtt att	2112			
Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile				

690	695	700	
cct cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc			2160
Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly			
705	710	715	
cta gat gca tca cag caa atc cgt ctg gaa gca gaa gaa gaa aaa tta			2208
Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu			
720	725	730	735
gct cat ttg cca ctc gct aaa aca gta tcc gta gaa gag ctt ctg caa			2256
Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln			
740	745	750	
tac gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg			2304
Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met			
755	760	765	
gct gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg			2352
Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu			
770	775	780	
ctt gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca			2400
Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr			
785	790	795	
atg ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc			2448
Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser			
800	805	810	815
gaa ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att			2496
Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile			
820	825	830	
tct tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc			2544
Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser			
835	840	845	
gtt gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att			2592
Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile			
850	855	860	
gcg tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc			2640
Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys			
865	870	875	
ttt att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa			2688
Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu			
880	885	890	895
acg ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga			2736
Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg			

900	905	910	
ggc ttt gtg cag gcg cgc aaa cag cta	aaa gaa caa gga cag tca ctt	2784	
Gly Phe Val Gln Ala Arg Lys Gln Leu	Lys Glu Gln Gly Gln Ser Leu		
915	920	925	
gga gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat	2832		
Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr			
930	935	940	
ctg tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg	2880		
Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr			
945	950	955	
ctt cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt	2928		
Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val			
960	965	970	
cag cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat	2976		
Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp			
980	985	990	
caa gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct	3024		
Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro			
995	1000	1005	
gcc gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg	3072		
Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val			
1010	1015	1020	
agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc	3120		
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly			
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cga tac gca aaa gac gtg tgg gct ggg taa	3150		
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1040	1045		

<210> 35

<211> 1048

<212> PRT

<213> Bacillus megaterium

<400> 35

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				20				25						30	

Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val

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35					40					45					
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Lys	Lys	Ala	His	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	Met
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Lys	Gly	Tyr	His	Ala	Met	Met	Val	Asp	Ile	Ala	Val	Gln	Leu	Val	Gln
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Lys	Trp	Glu	Arg	Leu	Asn	Ala	Asp	Glu	His	Ile	Glu	Val	Pro	Glu	Asp
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145					150					155					160
Arg	Phe	Asn	Ser	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	Ser
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Met	Val	Arg	Ala	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	Asn
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Pro	Asp	Asp	Pro	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	Asp
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Ile	Lys	Val	Met	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	Lys
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Ala	Ser	Gly	Glu	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	Gly
225						230					235				240
Lys	Asp	Pro	Glu	Thr	Gly	Glu	Pro	Leu	Asp	Asp	Glu	Asn	Ile	Arg	Tyr
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Gln	Ile	Ile	Thr	Phe	Leu	Ile	Ala	Gly	His	Glu	Thr	Thr	Ser	Gly	Leu
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Leu	Ser	Phe	Ala	Leu	Tyr	Phe	Leu	Val	Lys	Asn	Pro	His	Val	Leu	Gln
		275					280					285			
Lys	Ala	Ala	Glu	Glu	Ala	Ala	Arg	Val	Leu	Val	Asp	Pro	Val	Pro	Ser
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Tyr	Lys	Gln	Val	Lys	Gln	Leu	Lys	Tyr	Val	Gly	Met	Val	Leu	Asn	Glu
305					310					315				320	

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Ala	Leu	Arg	Leu	Trp	Pro	Thr	Ala	Pro	Ala	Phe	Ser	Leu	Tyr	Ala	Lys			
				325							330						335	
Glu	Asp	Thr	Val	Leu	Gly	Gly	Glu	Tyr	Pro	Leu	Glu	Lys	Gly	Asp	Glu			
				340							345						350	
Leu	Met	Val	Leu	Ile	Pro	Gln	Leu	His	Arg	Asp	Lys	Thr	Ile	Trp	Gly			
				355							360						365	
Asp	Asp	Val	Glu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Glu	Asn	Pro	Ser	Ala			
							375							380				
Ile	Pro	Gln	His	Ala	Phe	Lys	Pro	Phe	Gly	Asn	Gly	Gln	Arg	Ala	Cys			
385				390							395						400	
Ile	Gly	Gln	Gln	Phe	Ala	Leu	His	Glu	Ala	Thr	Leu	Val	Leu	Gly	Met			
				405							410						415	
Met	Leu	Lys	His	Phe	Asp	Phe	Glu	Asp	His	Thr	Asn	Tyr	Glu	Leu	Asp			
				420							425						430	
Ile	Lys	Glu	Thr	Leu	Thr	Leu	Lys	Pro	Glu	Gly	Phe	Val	Val	Lys	Ala			
				435							440						445	
Lys	Ser	Lys	Lys	Ile	Pro	Leu	Gly	Gly	Ile	Pro	Ser	Pro	Ser	Thr	Glu			
				450							455						460	
Gln	Ser	Ala	Lys	Lys	Val	Arg	Lys	Lys	Ala	Glu	Asn	Ala	His	Asn	Thr			
465				470							475						480	
Pro	Leu	Leu	Val	Leu	Tyr	Gly	Ser	Asn	Met	Gly	Thr	Ala	Glu	Gly	Thr			
				485							490						495	
Ala	Arg	Asp	Leu	Ala	Asp	Ile	Ala	Met	Ser	Lys	Gly	Phe	Ala	Pro	Gln			
				500							505						510	
Val	Ala	Thr	Leu	Asp	Ser	His	Ala	Gly	Asn	Leu	Pro	Arg	Glu	Gly	Ala			
				515							520						525	
Val	Leu	Ile	Val	Thr	Ala	Ser	Tyr	Asn	Gly	His	Pro	Pro	Asp	Asn	Ala			
				530							535						540	
Lys	Gln	Phe	Val	Asp	Trp	Leu	Asp	Gln	Ala	Ser	Ala	Asp	Glu	Val	Lys			
545				550							555						560	
Gly	Val	Arg	Tyr	Ser	Val	Phe	Gly	Cys	Gly	Asp	Lys	Asn	Trp	Ala	Thr			
				565							570						575	
Thr	Tyr	Gln	Lys	Val	Pro	Ala	Phe	Ile	Asp	Glu	Thr	Leu	Ala	Ala	Lys			
				580							585						590	
Gly	Ala	Glu	Asn	Ile	Ala	Asp	Arg	Gly	Glu	Ala	Asp	Ala	Ser	Asp	Asp			

595					600					605					
Phe	Glu	Gly	Thr	Tyr	Glu	Glu	Trp	Arg	Glu	His	Met	Trp	Ser	Asp	Val
610					615					620					
Ala	Ala	Tyr	Phe	Asn	Leu	Asp	Ile	Glu	Asn	Ser	Glu	Asp	Asn	Lys	Ser
625					630					635					640
Thr	Leu	Ser	Leu	Gln	Phe	Val	Asp	Ser	Ala	Ala	Asp	Met	Pro	Leu	Ala
				645					650					655	
Lys	Met	His	Gly	Ala	Phe	Ser	Thr	Asn	Val	Val	Ala	Ser	Lys	Glu	Leu
			660					665					670		
Gln	Gln	Pro	Gly	Ser	Ala	Arg	Ser	Thr	Arg	His	Leu	Glu	Ile	Glu	Leu
			675					680					685		
Pro	Lys	Glu	Ala	Ser	Tyr	Gln	Glu	Gly	Asp	His	Leu	Gly	Val	Ile	Pro
			690					695					700		
Arg	Asn	Tyr	Glu	Gly	Ile	Val	Asn	Arg	Val	Thr	Ala	Arg	Phe	Gly	Leu
705					710					715					720
Asp	Ala	Ser	Gln	Gln	Ile	Arg	Leu	Glu	Ala	Glu	Glu	Glu	Lys	Leu	Ala
				725					730					735	
His	Leu	Pro	Leu	Ala	Lys	Thr	Val	Ser	Val	Glu	Glu	Leu	Leu	Gln	Tyr
			740					745					750		
Val	Glu	Leu	Gln	Asp	Pro	Val	Thr	Arg	Thr	Gln	Leu	Arg	Ala	Met	Ala
			755					760					765		
Ala	Lys	Thr	Val	Cys	Pro	Pro	His	Lys	Val	Glu	Leu	Glu	Ala	Leu	Leu
			770					775					780		
Glu	Lys	Gln	Ala	Tyr	Lys	Glu	Gln	Val	Leu	Ala	Lys	Arg	Leu	Thr	Met
785					790					795					800
Leu	Glu	Leu	Leu	Glu	Lys	Tyr	Pro	Ala	Cys	Glu	Met	Lys	Phe	Ser	Glu
				805					810					815	
Phe	Ile	Ala	Leu	Leu	Pro	Ser	Ile	Arg	Pro	Arg	Tyr	Tyr	Ser	Ile	Ser
			820					825					830		
Ser	Ser	Pro	Arg	Val	Asp	Glu	Lys	Gln	Ala	Ser	Ile	Thr	Val	Ser	Val
			835					840					845		
Val	Ser	Gly	Glu	Ala	Trp	Ser	Gly	Tyr	Gly	Glu	Tyr	Lys	Gly	Ile	Ala
			850					855					860		
Ser	Asn	Tyr	Leu	Ala	Glu	Leu	Gln	Glu	Gly	Asp	Thr	Ile	Thr	Cys	Phe
865					870					875					880

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Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
 885 890 895

Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
 900 905 910

Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly
 915 920 925

Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
 930 935 940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
 945 950 955 960

His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
 965 970 975

His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
 980 985 990

Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
 995 1000 1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser
 1010 1015 1020

Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly Arg
 1025 1030 1035 1040

Tyr Ala Lys Asp Val Trp Ala Gly
 1045

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